

Table S16. Community gene clusters differentially expressed in the ceca of humanized mice fed the Western diet relative to the LF/PP diet.

Gene	Fold change	Genes	Annotation
Cluster54045	182.1	Csci3106 Dfor2481 Dlon0471	COG1653 ABC-type sugar transport system, periplasmic component
Cluster26863	102.9	SB23peg2545	COG3497 Phage tail sheath protein FI
Cluster205160	93.7	BVU3142 BVU3487 Bdor4466	
Cluster60857	72.5	Casp2879	COG1879 ABC-type sugar transport system, periplasmic component COG4213 ABC-type xylose transport system, periplasmic component
Cluster51636	72.2	SB23peg1618	COG1653 ABC-type sugar transport system, periplasmic component
Cluster213035	70.6	SB23peg3176	
Cluster31603	65.6	SB23peg2539	
Cluster153349	59.2	Csci3894	
Cluster7844	57.3	Bcoproc0991 Bple3463 BactD10295 Bthe3732261	COG3451 Type IV secretory pathway, VirB4 components
Cluster11578	45.3	BWH24249 Bcel2909	COG3693 Beta-1,4-xylanase COG5297 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
Cluster203859	44.9	BFych463590 BFnctc3394	
Cluster69732	43.3	Rtor0230	
Cluster119765	41.6	SB23peg1766	
Cluster66133	40.3	BVU3107 Bdor2554	COG4822 Cobalamin biosynthesis protein CbiK, Co2+ chelatase
Cluster51809	39.3	EUBREC0477 Bhan1249 Cnex0917 Ehal1451 Rtor1782	COG1879 ABC-type sugar transport system, periplasmic component
Cluster28481	37.1	SB23peg2795	COG3318 Predicted metal-binding protein related to the C-terminal domain of SecA
Cluster4687	36.3	Buni3038	COG4771 Outer membrane receptor for ferrienterochelin and colicins
Cluster33321	36.2	BDI2945	
Cluster19991	36.0	SB23peg2556	
Cluster128427	35.4	SB23peg2540	
Cluster205	35.1	Bhan1571	COG5492 Bacterial surface proteins containing Ig-like domains COG5263 FOG: Glucan-binding domain (YG repeat)
Cluster82603	34.8	SB23peg2552	
Cluster7643	32.9	SB23peg48	COG0574 Phosphoenolpyruvate synthase/pyruvate phosphate dikinase COG1080 Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria) COG3412 Uncharacterized protein conserved in bacteria COG2190 Phosphotransferase system IIA components
Cluster52272	30.9	SB23peg2541	
Cluster70111	30.7	BVU2445 Bdor3495	COG0639 Diadenosine tetraphosphatase and related serine/threonine protein phosphatases
Cluster187865	29.9	SB23peg2547	
Cluster91340	29.7	Cspi0131 Edo11738 SB23peg2652 Rtor1578	COG3716 Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID
Cluster44841	29.3	BWH24248 Bcel2910	
Cluster69363	29.1	Rtor0231	
Cluster53089	29.0	Bcoproc0995 Bple3459 BactD10291 Bthe3732266	
Cluster6842	28.5	SB23peg2555	
Cluster217843	28.2	Chyl3483	COG1278 Cold shock proteins
Cluster28004	28.2	BWH24247 Bcel2911 Bcel2913	
Cluster169921	27.8	SB23peg2542	
Cluster39467	27.7	Bcoproc0997 Bple3457 BactD10289 Bthe3732152 Bthe3732269	
Cluster3347	27.2	BDI2944	COG4771 Outer membrane receptor for ferrienterochelin and colicins COG1629 Outer membrane receptor proteins, mostly Fe transport COG4206 Outer membrane cobalamin receptor protein COG2304 Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
Cluster47585	26.1	Bryfor1338	COG0439 Biotin carboxylase COG4770 Acetyl/propionyl-CoA carboxylase, alpha subunit
Cluster19691	25.8	SB23peg706	COG1902 NADH:flavin oxidoreductases, Old Yellow Enzyme family
Cluster3191	25.7	SB23peg3941	COG2202 FOG: PAS/PAC domain COG3300 MHYT domain (predicted integral membrane sensor domain) COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG2200 FOG: EAL domain COG3614 Predicted periplasmic ligand-binding sensor domain
Cluster76297	25.6	Bcoproc0996 Bple3458 BactD10290 Bthe3732268	
Cluster122318	24.4	Edo11737 SB23peg2651 SB23peg2656	COG3715 Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIC COG3716 Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID
Cluster26278	24.3	SB23peg2710	COG4624 Iron only hydrogenase large subunit, C-terminal domain COG3383 Uncharacterized anaerobic dehydrogenase COG1034 NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G) COG0243 Anaerobic dehydrogenases, typically selenocysteine-containing

Cluster2470	24.2	Edol1314 SB23peg1107	COG1014 Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit COG1013 Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit COG0674 Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit
Cluster2540	24.1	DpigATC2091 DpigGOR11652	COG0587 DNA polymerase III, alpha subunit
Cluster11189	24.1	SB23peg2932	COG1882 Pyruvate-formate lyase
Cluster68544	23.9	Edol1599 SB23peg1427	COG0126 3-phosphoglycerate kinase COG0149 Triosephosphate isomerase
Cluster27820	23.8	Edol1685 SB23peg2603	COG1109 Phosphomannomutase
Cluster205742	23.8	BactD10297 Bthe3732260	
Cluster158239	23.7	Fuso41131324	COG0457 FOG: TPR repeat
Cluster55254	23.4	Csci1580	COG1653 ABC-type sugar transport system, periplasmic component COG2182 Maltose-binding periplasmic proteins/domains
Cluster132365	23.2	SB23peg209	COG1349 Transcriptional regulators of sugar metabolism
Cluster47976	23.2	Chir0726 Csci3423	COG3104 Dipeptide/tripeptide permease
Cluster126265	22.4	DpigATC2097 DpigGOR11658	COG4822 Cobalamin biosynthesis protein CbiK, Co ²⁺ chelataase
Cluster158256	22.3	SB23peg1003	
Cluster152720	21.6	BactD10285	
Cluster33993	21.5	Bhan0507	COG5492 Bacterial surface proteins containing Ig-like domains COG5263 FOG: Glucan-binding domain (YG repeat)
Cluster135606	21.3	Csci3359	COG4624 Iron only hydrogenase large subunit, C-terminal domain COG3383 Uncharacterized anaerobic dehydrogenase COG1034 NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G) COG0243 Anaerobic dehydrogenases, typically selenocysteine-containing
Cluster7000	21.3	Cbar1895	
Cluster155866	20.7	Bryfor1315	COG0110 Acetyltransferase (isoleucine patch superfamily) COG1045 Serine acetyltransferase COG2171 Tetrahydrodipicolinate N-succinyltransferase COG1605 Chorismate mutase
Cluster180921	20.7	Ebif0029 SB23peg2650	COG3444 Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB
Cluster161108	20.1	Csci2651	
Cluster199907	20.1	BactD10298 Bthe3732259	
Cluster130060	19.5	SB23peg2550	
Cluster37587	19.2	BVU2693 Bdor3774	
Cluster14996	18.7	Rtor1538	
Cluster30951	18.4	Aput1183	
Cluster59600	18.3	Bhan2717 Csym3389	COG1228 Imidazolonepropionase and related amidohydrolases
Cluster53148	17.7	Csci1520	COG1301 Na ⁺ /H ⁺ -dicarboxylate symporters COG3633 Na ⁺ /serine symporter
Cluster29304	17.4	SB23peg2442	COG0497 ATPase involved in DNA repair
Cluster74473	17.2	Bcap0088	COG1104 Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes
Cluster204075	16.9	Csci1192	
Cluster34783	16.8	Ebif0869 Edol1522 SB23peg3636	COG4670 Acyl CoA:acetate/3-ketoacid CoA transferase COG2057 Acyl CoA:acetate/3-ketoacid CoA transferase, beta subunit COG1788 Acyl CoA:acetate/3-ketoacid CoA transferase, alpha subunit
Cluster76015	16.8	Chyl3169 Csci3940 Dlon0626	COG0686 Alanine dehydrogenase
Cluster111656	16.6	SB23peg2935	COG0564 Pseudouridylyl synthases, 23S RNA-specific
Cluster45450	16.4	Csci1584	COG1362 Aspartyl aminopeptidase
Cluster2164	16.0	Cbol0851	COG5263 FOG: Glucan-binding domain (YG repeat)
Cluster21567	15.9	Csym4854	COG0405 Gamma-glutamyltransferase
Cluster111319	15.9	Aput2282	
Cluster649	15.8	SB23peg3089	
Cluster104623	15.6	Edol1722 SB23peg2630	COG0526 Thiol-disulfide isomerase and thioredoxins COG0492 Thioredoxin reductase
Cluster33185	15.6	Aput1824	
Cluster200291	15.5	BactD10286 Bthe3732157	
Cluster136195	15.3	Csym3424	COG2968 Uncharacterized conserved protein
Cluster15611	15.3	Ebif1827 Edol0428 SB23peg882	COG0480 Translation elongation factors (GTPases)
Cluster88063	15.3	SB23peg1526	
Cluster146545	15.2	SB23peg873	COG0087 Ribosomal protein L3
Cluster99330	15.2	Bryfor0853	COG1045 Serine acetyltransferase COG2151 Predicted metal-sulfur cluster biosynthetic enzyme
Cluster100079	14.8	SB23peg2639	COG0391 Uncharacterized conserved protein
Cluster16138	14.7	BVU3108 Bdor2553 Bste0510	COG4771 Outer membrane receptor for ferrienterochelin and colicins COG1629 Outer membrane receptor proteins, mostly Fe transport COG4206 Outer membrane cobalamin receptor protein
Cluster635	14.7	Rtor0725	COG4886 Leucine-rich repeat (LRR) protein
Cluster36006	14.6	Cbar2121	
Cluster118136	14.5	SB23peg1524	COG3623 Putative L-xylulose-5-phosphate 3-epimerase
Cluster5443	14.4	Csci2644	

Cluster73231	14.3	Edol0066 SB23peg1137	COG1820 N-acetylglucosamine-6-phosphate deacetylase
Cluster79220	14.2	Vvad5480829	
Cluster142754	14.2	SB23peg693 SB23peg1525	COG0235 Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases
Cluster25509	14.2	Fuso41130728	COG1132 ABC-type multidrug transport system, ATPase and permease components
Cluster201529	14.2	Casp1399	
Cluster160342	13.8	Svar2229	COG0110 Acetyltransferase (isoleucine patch superfamily) COG1605 Chorismate mutase
Cluster137678	13.5	Cbol2964	
Cluster4974	13.3	Aput0215	COG0342 Preprotein translocase subunit SecD COG0341 Preprotein translocase subunit SecF
Cluster209891	13.1	Acol3126	
Cluster78424	13.0	Edol1098 SB23peg3978	COG0206 Cell division GTPase
Cluster37375	12.8	Vvad5480667	
Cluster100666	12.7	BVU2243 Bdor3144	COG4874 Uncharacterized protein conserved in bacteria containing a penten-type domain
Cluster76495	12.6	Casp0290 SB23peg1530	COG2220 Predicted Zn-dependent hydrolases of the beta-lactamase fold
Cluster187370	12.6	Csym2975	
Cluster128612	12.6	Aput1080	
Cluster192693	12.5	Rtor0239	COG2050 Uncharacterized protein, possibly involved in aromatic compounds catabolism
Cluster186975	12.5	SB23peg2827	COG0102 Ribosomal protein L13
Cluster135924	12.5	Aput1553	
Cluster193328	12.4	Chyl2948 Cnex2220 Csci2181 Dlon0165	
Cluster69680	12.4	SB23peg3655	COG4992 Ornithine/acetylornithine aminotransferase
Cluster93494	12.4	Csci2426	COG0524 Sugar kinases, ribokinase family COG2771 DNA-binding HTH domain-containing proteins COG3892 Uncharacterized protein conserved in bacteria
Cluster219821	12.3	Bcap0565	COG1278 Cold shock proteins
Cluster114618	12.1	Aput1168	COG0575 CDP-diglyceride synthetase COG4589 Predicted CDP-diglyceride synthetase/phosphatidate cytidyltransferase
Cluster26407	12.1	SB23peg911	COG1132 ABC-type multidrug transport system, ATPase and permease components
Cluster164663	11.8	SB23peg3643	COG0778 Nitroreductase
Cluster8797	11.8	BVU3098 BFych462693 BFnctc2713 BWH25274 Bdor2561 Bfra31123581	COG0209 Ribonucleotide reductase, alpha subunit
Cluster52906	11.8	SB23peg2936	COG2202 FOG: PAS/PAC domain COG3322 Predicted periplasmic ligand-binding sensor domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG2199 FOG: GGDEF domain COG2200 FOG: EAL domain COG3614 Predicted periplasmic ligand-binding sensor domain COG2703 Hemerythrin
Cluster137478	11.8	BVU3955 Bdor0775	COG1051 ADP-ribose pyrophosphatase
Cluster54795	11.7	BDI1956	COG0577 ABC-type antimicrobial peptide transport system, permease component
Cluster34379	11.5	Csym3970	COG2082 Precorrin isomerase COG2897 Rhodanese-related sulfurtransferase COG0425 Predicted redox protein, regulator of disulfide bond formation COG0155 Sulfite reductase, beta subunit (hemoprotein)
Cluster20662	11.5	Bdor1912	COG1506 Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
Cluster116375	11.5	Csci2274 Dlon1232	COG1760 L-serine deaminase
Cluster166155	11.3	BFych462537 BFnctc2566	
Cluster16125	11.3	Aput0023	COG0532 Translation initiation factor 2 (IF-2; GTPase)
Cluster25786	11.3	BDI1290	COG0358 DNA primase (bacterial type)
Cluster148082	11.0	BDI1495 PRABACTJOHN2577 Pmer3274	COG0564 Pseudouridylyl synthases, 23S RNA-specific
Cluster159182	11.0	Csym1508	
Cluster143918	10.9	SB23peg840	
Cluster109967	10.9	Edol0892 SB23peg1876	COG0264 Translation elongation factor Ts
Cluster46415	10.9	BDI0397	COG1453 Predicted oxidoreductases of the aldo/keto reductase family COG0667 Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)
Cluster110337	10.9	Bfin0425 Bova4114 Bsp1161655 BactD10242 Bthe3733776 Buni2603	
Cluster9600	10.8	Rtor2052	
Cluster34304	10.7	Aput0257	COG2025 Electron transfer flavoprotein, alpha subunit COG1960 Acyl-CoA dehydrogenases
Cluster18102	10.6	Csci2425	
Cluster210081	10.6	Csci3509	
Cluster159954	10.6	Acol2900	COG1595 DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog
Cluster57621	10.6	SB23peg2245	COG0544 FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)
Cluster52165	10.4	Ceut1129 CspL21823 Dfor1934 Dlon0446 Even1013 Rlac2149	COG1879 ABC-type sugar transport system, periplasmic component
Cluster14454	10.3	Bcap1077	COG1185 Polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase)
Cluster508	10.3	Bhan1626	COG5492 Bacterial surface proteins containing Ig-like domains COG3525 N-acetyl-beta-hexosaminidase COG5263 FOG: Glucan-binding domain (YG repeat)
Cluster120258	10.2	Ebif0755 Edol0423 Hfil1209 SB23peg870	COG0090 Ribosomal protein L2
Cluster12579	10.1	SB23peg1048	COG0058 Glucan phosphorylase

Cluster97629	10.1	SB23peg247	COG1482 Phosphomannose isomerase
Cluster55321	10.1	Edol0895 SB23peg1879	COG0445 NAD/FAD-utilizing enzyme apparently involved in cell division COG1206 NAD(FAD)-utilizing enzyme possibly involved in translation
Cluster103092	10.0	Csci3553	COG1940 Transcriptional regulator/sugar kinase
Cluster12049	10.0	SB23peg755	COG0342 Preprotein translocase subunit SecD COG0341 Preprotein translocase subunit SecF
Cluster14520	10.0	Aput2067	COG1506 Dipeptidyl aminopeptidases/acylaminoacyl-peptidases
Cluster175895	10.0	Rtor2511	
Cluster57681	9.9	Casp1013 Cbol0349 Cbol1238 Cbol4074 Cbol4080 Cbol6581 Ccom1194 CspL21956 Csym0303 Dfor1913 Robe2705 Robe2706 Rtor0134 Rtor0268	COG3328 Transposase and inactivated derivatives
Cluster145423	9.9	Csym3422	COG1555 DNA uptake protein and related DNA-binding proteins
Cluster24049	9.8	Aput1420	
Cluster29286	9.8	Csym4434	
Cluster100829	9.7	Bhan0551	COG4086 Predicted secreted protein
Cluster34859	9.7	Aput0931	
Cluster221185	9.6	Csym0054	
Cluster58022	9.6	BDI1965	
Cluster229633	9.5	RintL12834	
Cluster21762	9.4	SB23peg2604	COG0296 1,4-alpha-glucan branching enzyme
Cluster7680	9.3	SB23peg2702	COG0474 Cation transport ATPase
Cluster65144	9.2	Aput1526	COG2081 Predicted flavoproteins
Cluster17600	9.2	SB23peg3986	COG1200 RecG-like helicase
Cluster161177	9.2	Edol0909 SB23peg1907	COG0522 Ribosomal protein S4 and related proteins
Cluster14745	9.2	SB23peg196	COG1721 Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) COG1305 Transglutaminase-like enzymes, putative cysteine proteases
Cluster46453	9.1	Aput0520	
Cluster114438	9.1	SB23peg4271	COG0191 Fructose/tagatose bisphosphate aldolase
Cluster218129	9.1	L0366 Ldb0418 LSEI2481 SB23peg851	COG0361 Translation initiation factor 1 (IF-1) COG0421 Spermidine synthase
Cluster96472	9.0	Aput1345	COG0753 Catalase
Cluster75137	9.0	BWH21063 Bcel3434 Bint1781	COG0463 Glycosyltransferases involved in cell wall biogenesis COG0438 Glycosyltransferase
Cluster6115	8.9	Edol1719 Hfil0174 Hfil0175 SB23peg2627	COG0178 Excinuclease ATPase subunit
Cluster209028	8.9	Acol2899	
Cluster99075	8.9	SB23peg1912	COG1079 Uncharacterized ABC-type transport system, permease component
Cluster84408	8.9	Aput2323	COG0526 Thiol-disulfide isomerase and thioredoxins COG0785 Cytochrome c biogenesis protein
Cluster106600	8.9	BactD14416 Bxyl1721	COG0584 Glycerophosphoryl diester phosphodiesterase COG1409 Predicted phosphohydrolases
Cluster219785	8.8	Aput0848	COG1053 Succinate dehydrogenase/fumarate reductase, flavoprotein subunit
Cluster69824	8.8	Aput0468	
Cluster138420	8.8	SB23peg231	COG2188 Transcriptional regulators
Cluster28887	8.8	SB23peg2097	COG0028 Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
Cluster5142	8.8	Bova0683 BactD14411 Bxyl1726	COG4771 Outer membrane receptor for ferrienterochelin and colicins
Cluster76264	8.8	Aput1549	
Cluster226631	8.8	Csci3814	
Cluster44978	8.7	Ebif0702 Edol0597 Hfil0661 SB23peg1252	COG0055 F0F1-type ATP synthase, beta subunit
Cluster122839	8.7	SB23peg3479	
Cluster314	8.7	Rtor1355	COG4409 Neuraminidase (sialidase)
Cluster102874	8.7	Aput1921	COG1162 Predicted GTPases
Cluster107585	8.7	Bcap0278	COG1131 ABC-type multidrug transport system, ATPase component COG4152 ABC-type uncharacterized transport system, ATPase component
Cluster80585	8.7	Edol1283 SB23peg1577	COG0208 Ribonucleotide reductase, beta subunit
Cluster103656	8.7	Csym4653	COG0726 Predicted xylanase/chitin deacetylase COG3858 Predicted glycosyl hydrolase COG4249 Uncharacterized protein containing caspase domain
Cluster166643	8.7	EUBREC0801 EUBREC2694 Hfil2896	
Cluster40486	8.7	Aput1419	
Cluster19893	8.6	SB23peg4188	COG1269 Archaeal/vacuolar-type H ⁺ -ATPase subunit I
Cluster204975	8.6	Csci0949	
Cluster21074	8.6	Aput2010	COG3408 Glycogen debranching enzyme
Cluster20395	8.6	Aput1727	COG1022 Long-chain acyl-CoA synthetases (AMP-forming)
Cluster212075	8.6	Hfil1215 SB23peg864	COG0186 Ribosomal protein S17
Cluster218091	8.5	BFych464401	
Cluster49599	8.5	SB23peg2929	
Cluster16870	8.4	BVU4051 Bdor0701	COG1649 Uncharacterized protein conserved in bacteria
Cluster73384	8.4	Aput0104	

Cluster87821	8.4	Bcoproc1000 Bple3454 BactD10282 Bthe3732160	
Cluster59719	8.3	SB23peg4182	COG0569 K ⁺ transport systems, NAD-binding component COG0589 Universal stress protein UspA and related nucleotide-binding proteins COG0475 Kef-type K ⁺ transport systems, membrane components COG1226 Kef-type K ⁺ transport systems, predicted NAD-binding component COG1762 Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)
Cluster60047	8.3	Rtor2286	COG1879 ABC-type sugar transport system, periplasmic component
Cluster107923	8.3	PRABACTJOHN2984	
Cluster59498	8.3	BFych462631 BFnctc2652 Bfra31124339	
Cluster16096	8.2	SB23peg4022	COG0768 Cell division protein FtsI/penicillin-binding protein 2
Cluster24929	8.2	SB23peg2388	COG0358 DNA primase (bacterial type)
Cluster94477	8.2	SB23peg2534	
Cluster64459	8.2	Aput1259	
Cluster86038	8.2	Aput1184	
Cluster200564	8.2	BFych462357 BFnctc2442	
Cluster48132	8.1	BVU1597 Buni1938 Pmer2578	
Cluster87518	8.1	Csci0495	COG1686 D-alanyl-D-alanine carboxypeptidase
Cluster21572	8.0	Ebif1032 Edol1400 SB23peg2313	COG1217 Predicted membrane GTPase involved in stress response
Cluster67535	8.0	BVU1312 Bdor1949	COG0500 SAM-dependent methyltransferases
Cluster146755	7.9	BT0694 BFych462154 BFych462156 BFnctc2211 BFnctc2213 BDI1637 BWH22057 Bcac2632 Bcel3908 Bfra31123958 Bfra31123960 Bint2173 Bova1789 Bsp1163844 BactD11802 BactD20587 Bste2351 Bthe3735636 Bthe7334170 Buni1519 Bxyl0220 PRABACTJOHN0006 PRABACTJOHN0957 Pmer0367 Pmer1866	COG1136 ABC-type antimicrobial peptide transport system, ATPase component COG4181 Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis, ATPase component COG2884 Predicted ATPase involved in cell division
Cluster4323	7.9	BDI0336 PRABACTJOHN2603 Pmer3300	COG0841 Cation/multidrug efflux pump
Cluster124518	7.9	Aput0846	
Cluster77551	7.8	Csci2048	
Cluster132578	7.8	Aput1697	
Cluster19623	7.8	Acol2707	COG1297 Predicted membrane protein
Cluster207144	7.8	SB23peg1507	COG0360 Ribosomal protein S6
Cluster9500	7.8	Aput0902	COG0542 ATPases with chaperone activity, ATP-binding subunit
Cluster75314	7.8	Csym4386	COG2358 TRAP-type uncharacterized transport system, periplasmic component
Cluster208459	7.8	SB23peg2417	COG0776 Bacterial nucleoid DNA-binding protein
Cluster87096	7.8	CspM6212593 Csym3947	COG1186 Protein chain release factor B
Cluster74254	7.7	b1128 EFER1802 Csp1987 Ecan1863 ShigspD93103	COG2850 Uncharacterized conserved protein
Cluster100569	7.7	SB23peg2453	COG0196 FAD synthase
Cluster41839	7.7	EUBREC3196 Ccom0190 CspL21798 Dlon1529 Eeli0796 Rlac2034 Robe1518	COG1115 Na ⁺ /alanine symporter
Cluster10759	7.7	Aput0973	COG0787 Alanine racemase
Cluster59516	7.6	BDI1084	COG0402 Cytosine deaminase and related metal-dependent hydrolases
Cluster16509	7.5	Rtor0576	COG0515 Serine/threonine protein kinase COG2815 Uncharacterized protein conserved in bacteria COG5616 Predicted integral membrane protein
Cluster30463	7.5	SB23peg1102	COG1227 Inorganic pyrophosphatase/exopolyphosphatase
Cluster209816	7.4	BFych463449 BFnctc3268	
Cluster97586	7.4	Ebif0775 Edol0182 SB23peg2154	COG0205 6-phosphofructokinase
Cluster27358	7.4	BDI3774	COG0366 Glycosidases
Cluster10836	7.4	BDI0768	
Cluster105450	7.4	BVU1319 Bdor1956	COG0280 Phosphotransacetylase COG2030 Acyl dehydratase COG0857 BioD-like N-terminal domain of phosphotransacetylase
Cluster103492	7.4	Bhan0505	COG0526 Thiol-disulfide isomerase and thioredoxins COG0492 Thioredoxin reductase
Cluster6388	7.4	BDI0390	COG4771 Outer membrane receptor for ferrienterochelin and colicins COG1629 Outer membrane receptor proteins, mostly Fe transport COG4206 Outer membrane cobalamin receptor protein
Cluster182806	7.3	SB23peg2048	

Cluster11205	7.3	Aput1185	COG0060 Isoleucyl-tRNA synthetase COG0525 Valyl-tRNA synthetase
Cluster7591	7.3	Rtor0676	COG0419 ATPase involved in DNA repair
Cluster19140	7.3	b0879 EFER1027 Csp2974 Ecan1627 ShigspD90413	COG1136 ABC-type antimicrobial peptide transport system, ATPase component COG0577 ABC-type antimicrobial peptide transport system, permease component
Cluster214948	7.3	SB23peg1804	
Cluster188533	7.3	Aput0765	COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains COG1221 Transcriptional regulators containing an AAA-type ATPase domain and a DNA-binding domain COG3604 Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains COG3829 Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains COG3284 Transcriptional activator of acetoin/glycerol metabolism COG3283 Transcriptional regulator of aromatic amino acids metabolism
Cluster67599	7.3	Aput0982	COG1853 Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family COG0446 Uncharacterized NAD(FAD)-dependent dehydrogenases COG1773 Rubredoxin COG0426 Uncharacterized flavoproteins
Cluster66371	7.3	Edol0790 SB23peg2389	COG0568 DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32)
Cluster148702	7.2	BVU1692 Bdor0287	
Cluster211107	7.2	SB23peg2600	COG1925 Phosphotransferase system, HPr-related proteins
Cluster88519	7.2	SB23peg3869	COG1408 Predicted phosphohydrolases
Cluster6576	7.2	BDI1508	COG4771 Outer membrane receptor for ferrienterochelin and colicins COG1629 Outer membrane receptor proteins, mostly Fe transport
Cluster68065	7.2	BDI2465 Buni0047	
Cluster63450	7.1	Aput0345	
Cluster37585	7.0	BT2690 BVU0338 BFyc h464144 BFnctc3966 BDI3648 BWH20039 Bcel2311 Bdor0094 Begg2597 Bfra31120800 Bint1714 Bova0732 Bsp1160049 BactD14483 BactD20057 Bste2261 Bthe3731259 Bthe7330405 Buni0593 Bxy11650 PRABACTJOHN3703 Pmer1234	COG2986 Histidine ammonia-lyase
Cluster39461	7.0	Bcap1262	
Cluster175358	7.0	Hfil1222 SB23peg856	COG0098 Ribosomal protein S5
Cluster92155	7.0	Csym3974	
Cluster73560	7.0	Csym1892	COG0330 Membrane protease subunits, stomatin/prohibitin homologs
Cluster19487	6.9	Bcap1540	COG0539 Ribosomal protein S1 COG0761 Penicillin tolerance protein
Cluster15726	6.9	Chyl12747 Csci3112	
Cluster139291	6.9	Casp1073	COG0363 6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase
Cluster172268	6.9	FpraM2121084	COG0330 Membrane protease subunits, stomatin/prohibitin homologs
Cluster35883	6.9	SB23peg113	
Cluster28656	6.9	Aput0312	
Cluster126960	6.9	BVU0044 Bdor0472	COG3507 Beta-xylosidase COG2273 Beta-glucanase/Beta-glucan synthetase COG3693 Beta-1,4-xylanase COG3291 FOG: PKD repeat COG2931 RTX toxins and related Ca2+-binding proteins
Cluster142989	6.9	Aput0682	
Cluster154928	6.9	Casp1614	
Cluster125189	6.9	Cnex1102	COG3267 Type II secretory pathway, component ExeA (predicted ATPase)
Cluster169505	6.9	Rtor2547	
Cluster54039	6.9	Csci1212	COG1003 Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain COG0403 Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain
Cluster49545	6.9	Csym4785	
Cluster30655	6.8	Acol0189	COG1961 Site-specific recombinases, DNA invertase Pin homologs
Cluster90303	6.8	Csym3985	
Cluster12324	6.8	SB23peg3451	COG1132 ABC-type multidrug transport system, ATPase and permease components
Cluster38084	6.8	Csci3478	COG1492 Cobyrinic acid synthase
Cluster119969	6.8	Aput0959	COG3176 Putative hemolysin
Cluster19597	6.7	Edol0756 SB23peg2338	COG0187 Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Cluster33033	6.7	BDI0362	COG3119 Arylsulfatase A and related enzymes
Cluster4119	6.6	Csym4446	COG0463 Glycosyltransferases involved in cell wall biogenesis COG1887 Putative glycosyl/glycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC COG1216 Predicted glycosyltransferases COG3754 Lipopolysaccharide biosynthesis protein COG0438 Glycosyltransferase COG3914 Predicted O-linked N-acetylglucosamine transferase, SPINDLY family COG1835 Predicted acyltransferases COG2374 Predicted extracellular nuclease
Cluster53025	6.6	Aput0594	COG3681 Uncharacterized conserved protein
Cluster70926	6.6	Aput1586	
Cluster39710	6.5	Casp0492	COG0747 ABC-type dipeptide transport system, periplasmic component COG4166 ABC-type oligopeptide transport system, periplasmic component
Cluster88433	6.5	Cbol6374 CspM6212533 Csym4296	COG2255 Holliday junction resolvase, helicase subunit
Cluster191022	6.5	SB23peg2383	COG0295 Cytidine deaminase
Cluster6872	6.5	Aput2284	

Cluster171431	6.5	SB23peg3443	COG1045 Serine acetyltransferase COG2151 Predicted metal-sulfur cluster biosynthetic enzyme
Cluster51106	6.5	SB23peg2707	COG0534 Na ⁺ -driven multidrug efflux pump
Cluster62187	6.5	Chyl1433 Csci3572	COG1541 Coenzyme F390 synthetase
Cluster213270	6.4	Bcap0100	
Cluster29740	6.4	EUBREC0479 Ehal1453	COG1879 ABC-type sugar transport system, periplasmic component COG1172 Ribose/xylose/arabinose/galactoside ABC-type transport systems, permease components COG4158 Predicted ABC-type sugar transport system, permease component COG4211 ABC-type glucose/galactose transport system, permease component COG4214 ABC-type xylose transport system, permease component
Cluster123838	6.4	SB23peg1523	COG0561 Predicted hydrolases of the HAD superfamily COG4696 Uncharacterized protein conserved in bacteria COG2050 Uncharacterized protein, possibly involved in aromatic compounds catabolism
Cluster107587	6.4	Bcap1093	COG4658 Predicted NADH:ubiquinone oxidoreductase, subunit RnfD COG1805 Na ⁺ -transporting NADH:ubiquinone oxidoreductase, subunit NqrB
Cluster2508	6.4	SB23peg695	COG5492 Bacterial surface proteins containing Ig-like domains COG4886 Leucine-rich repeat (LRR) protein
Cluster42269	6.4	Msm1570 Msmi741202 Msmi750477	COG0771 UDP-N-acetylmuramoylalanine-D-glutamate ligase COG0769 UDP-N-acetylmuramyl tripeptide synthase
Cluster64249	6.4	Chyl2143	COG1129 ABC-type sugar transport system, ATPase component
Cluster91773	6.4	SB23peg2441	COG0750 Predicted membrane-associated Zn-dependent proteases 1
Cluster181172	6.4	Aput1060	COG0167 Dihydroorotate dehydrogenase
Cluster10147	6.4	SB23peg2619	COG0058 Glucan phosphorylase
Cluster234804	6.4	Acol1792	
Cluster199960	6.4	Chyl0419 Csci0764	COG0662 Mannose-6-phosphate isomerase
Cluster65679	6.4	DpigATC1540 DpigGOR12333	COG1748 Saccharopine dehydrogenase and related proteins
Cluster177411	6.3	Bdor3030	COG0716 Flavodoxins
Cluster3324	6.3	SB23peg2813	COG4913 Uncharacterized protein conserved in bacteria
Cluster71974	6.3	Aput0873	
Cluster39136	6.3	Csci0514 Dlon2225	COG0621 2-methylthioadenine synthetase
Cluster5603	6.1	Aput1873	
Cluster25081	6.1	Aput1875	COG1032 Fe-S oxidoreductase
Cluster179378	6.1	Csci3357	COG1905 NADH:ubiquinone oxidoreductase 24 kD subunit
Cluster31179	6.1	DpigATC0512 DpigGOR11214	COG0459 Chaperonin GroEL (HSP60 family)
Cluster41835	6.0	EUBREC0889	COG2195 Di- and tripeptidases
Cluster66074	6.0	SB23peg1138	COG1853 Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family COG0446 Uncharacterized NAD(FAD)-dependent dehydrogenases COG1773 Rubredoxin COG0426 Uncharacterized flavoproteins
Cluster142201	6.0	SB23peg3447	COG1131 ABC-type multidrug transport system, ATPase component COG4152 ABC-type uncharacterized transport system, ATPase component
Cluster161215	6.0	SB23peg3364	COG0110 Acetyltransferase (isoleucine patch superfamily) COG1605 Chorismate mutase
Cluster17878	6.0	Csci0766	COG0577 ABC-type antimicrobial peptide transport system, permease component
Cluster7154	6.0	Csci3455	COG0577 ABC-type antimicrobial peptide transport system, permease component
Cluster45302	6.0	BVU1398 Bdor2047	COG0772 Bacterial cell division membrane protein
Cluster1944	6.0	Aput0870	COG0047 Phosphoribosylformylglycinamide (FGAM) synthase, glutamine amidotransferase domain COG0046 Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain
Cluster5187	6.0	BFych463146 BFnctc2981 Bfra31121454	COG0419 ATPase involved in DNA repair
Cluster135734	5.9	SB23peg3520	COG0543 2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases
Cluster105753	5.9	Edol0207 SB23peg2041	COG0564 Pseudouridylyl synthases, 23S RNA-specific
Cluster183295	5.9	SB23peg2817	
Cluster27951	5.9	SB23peg774	COG3436 Transposase and inactivated derivatives
Cluster29010	5.9	Csci0734	COG1523 Type II secretory pathway, pullulanase PulA and related glycosidases
Cluster6264	5.9	Acol0723	
Cluster116952	5.9	Csym2690	
Cluster82462	5.9	Casp2559 Cbol2708	COG2017 Galactose mutarotase and related enzymes
Cluster118140	5.9	SB23peg2793	COG1307 Uncharacterized protein conserved in bacteria COG1461 Predicted kinase related to dihydroxyacetone kinase
Cluster170276	5.9	Cbar1514 Cbar1516 Cbar1520 Chir0228 Chir1192	COG1592 Rubrerythrin
Cluster177237	5.9	Rtor1308	
Cluster177933	5.9	Casp4555 Cbol0939 Csym0746	COG1905 NADH:ubiquinone oxidoreductase 24 kD subunit
Cluster178954	5.9	Csym3230	COG0244 Ribosomal protein L10
Cluster31454	5.9	Csym3873	COG0784 FOG: CheY-like receiver COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains COG4753 Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain COG2197 Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain COG3279 Response regulator of the LytR/AlgR family COG2207 AraC-type DNA-binding domain-containing proteins COG4936 Predicted sensor domain

Cluster56258	5.9	Edol0984 SB23peg769	COG0536 Predicted GTPase
Cluster115282	5.9	Casp2938	COG0524 Sugar kinases, ribokinase family
Cluster70757	5.9	DpigATC2041 DpigGOR11319	COG1853 Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family COG0446 Uncharacterized NAD(FAD)-dependent dehydrogenases COG1773 Rubredoxin COG0426 Uncharacterized flavoproteins
Cluster114958	5.9	SB23peg3654	COG0548 Acetylglutamate kinase COG1364 N-acetylglutamate synthase (N-acetylornithine aminotransferase)
Cluster27230	5.8	Rtor1536	COG4624 Iron only hydrogenase large subunit, C-terminal domain COG3604 Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains COG3829 Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding domains COG2000 Predicted Fe-S protein
Cluster52273	5.8	SB23peg3054	COG2265 SAM-dependent methyltransferases related to tRNA (uracil-5-)-methyltransferase
Cluster80061	5.8	Bcap1339	COG0715 ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
Cluster16258	5.8	Aput0269	COG0178 Excinuclease ATPase subunit
Cluster2739	5.8	Bcap0447	COG1038 Pyruvate carboxylase COG0439 Biotin carboxylase
Cluster161641	5.8	Csym1542	
Cluster49756	5.8	Bgal1173	
Cluster63990	5.8	SB23peg3653	COG1364 N-acetylglutamate synthase (N-acetylornithine aminotransferase)
Cluster55160	5.7	Bdor3267	
Cluster104776	5.7	BVU4117 BFych461706 BFnctc1712 BDI2941 Bcac2903 Bcoprop1903 Bdor0619 Begg2061 Bfra31123364 Bova0191 Bpl e0537 Bste1565 Bxy10341 PRABACTJOHN0519 Pmer0262	COG0329 Dihydrodipicolinate synthase/N-acetylneuraminase lyase
Cluster200913	5.7	Rtor2129	
Cluster50529	5.6	Rumhyd0039	COG0334 Glutamate dehydrogenase/leucine dehydrogenase
Cluster61664	5.6	BFych464398	
Cluster39593	5.6	SB23peg2629	COG0546 Predicted phosphatases COG0682 Prolipoprotein diacylglyceryltransferase
Cluster65675	5.6	Casp3874 Ccom0852 Chyl3375 Csci1518 Dlon0982	COG0156 7-keto-8-aminopelargonate synthetase and related enzymes
Cluster67080	5.6	Edol0218 SB23peg2022	
Cluster124521	5.5	Aput2326	
Cluster307	5.5	CspL21240	COG3291 FOG: PKD repeat
Cluster54107	5.5	SB23peg4122	COG2270 Permeases of the major facilitator superfamily
Cluster72074	5.5	Cbol5748	COG0673 Predicted dehydrogenases and related proteins
Cluster81009	5.5	SB23peg3059	COG4851 Protein involved in sex pheromone biosynthesis
Cluster85253	5.5	Acol0814	
Cluster11468	5.5	Aput0457	COG1198 Primosomal protein N' (replication factor Y) - superfamily II helicase
Cluster55120	5.5	Aput0471	
Cluster142335	5.5	BVU3631 Bdor1367	COG1131 ABC-type multidrug transport system, ATPase component COG4555 ABC-type Na+ transport system, ATPase component COG4152 ABC-type uncharacterized transport system, ATPase component COG1125 ABC-type proline/glycine betaine transport systems, ATPase components COG1116 ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component COG4586 ABC-type uncharacterized transport system, ATPase component
Cluster162701	5.5	SB23peg2157	COG2320 Uncharacterized conserved protein COG0237 Dephospho-CoA kinase
Cluster174249	5.5	Bhan2715	COG3404 Methenyl tetrahydrofolate cyclohydrolase COG3643 Glutamate formiminotransferase
Cluster182547	5.5	Aput1696	COG2843 Putative enzyme of poly-gamma-glutamate biosynthesis (capsule formation)
Cluster110855	5.5	Bhan2278	COG0668 Small-conductance mechanosensitive channel COG3264 Small-conductance mechanosensitive channel
Cluster70033	5.5	SB23peg2125	
Cluster96284	5.5	SB23peg3540	COG0280 Phosphotransacetylase COG0857 BioD-like N-terminal domain of phosphotransacetylase
Cluster176884	5.5	Acol3457	COG1180 Pyruvate-formate lyase-activating enzyme COG0602 Organic radical activating enzymes
Cluster188169	5.5	Casp3031	COG1725 Predicted transcriptional regulators COG1167 Transcriptional regulators containing a DNA-binding HTH domain and an aminotransferase domain (MocR family) and their eukaryotic orthologs
Cluster28992	5.5	Casp5164	COG0572 Uridine kinase COG0441 Threonyl-tRNA synthetase
Cluster29364	5.5	Bhan0547	COG1227 Inorganic pyrophosphatase/exopolyphosphatase COG4109 Predicted transcriptional regulator containing CBS domains
Cluster32585	5.5	Csym1939	COG0784 FOG: CheY-like receiver COG2204 Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains COG4753 Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain COG2197 Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain COG3279 Response regulator of the LytR/AIgR family COG2207 AraC-type DNA-binding domain-containing proteins
Cluster48574	5.5	Casp5995	COG4260 Putative virion core protein (lumpy skin disease virus)
Cluster68160	5.5	Csym1490	COG1744 Uncharacterized ABC-type transport system, periplasmic component/surface lipoprotein
Cluster129098	5.5	BDI0777	

Cluster161180	5.4	Edol1435 SB23peg2201	COG0242 N-formylmethionyl-tRNA deformylase COG0194 Guanylate kinase
Cluster25367	5.4	Csci2643	COG2202 FOG: PAS/PAC domain COG3437 Response regulator containing a CheY-like receiver domain and an HD-GYP domain COG3300 MHYT domain (predicted integral membrane sensor domain) COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG2200 FOG: EAL domain
Cluster116031	5.4	SB23peg3087	COG4667 Predicted esterase of the alpha-beta hydrolase superfamily
Cluster67015	5.4	Cmet1064	COG0617 tRNA nucleotidyltransferase/poly(A) polymerase
Cluster119245	5.4	SB23peg1253	COG0224 F0F1-type ATP synthase, gamma subunit
Cluster344	5.3	BFych460786 BFnctc0713 Bfra31122521	COG2373 Large extracellular alpha-helical protein
Cluster134812	5.3	BFych461681 BFnctc1688 Bfra31123342	
Cluster113087	5.3	Ccom2157	COG1388 FOG: LysM repeat COG3409 Putative peptidoglycan-binding domain-containing protein COG3103 SH3 domain protein COG0791 Cell wall-associated hydrolases (invasion-associated proteins) COG3883 Uncharacterized protein conserved in bacteria COG3209 Rhs family protein
Cluster143915	5.3	SB23peg226	COG0274 Deoxyribose-phosphate aldolase
Cluster17956	5.2	Edol0622 SB23peg3704	COG0187 Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit
Cluster370	5.2	BDI3747	COG2373 Large extracellular alpha-helical protein
Cluster54708	5.2	SB23peg1850	COG0773 UDP-N-acetylmuramate-alanine ligase COG1181 D-alanine-D-alanine ligase and related ATP-grasp enzymes
Cluster240563	5.2	Csci2836	
Cluster148254	5.2	Aput0948	
Cluster98183	5.2	FpraM2120253 Svar1456	COG0202 DNA-directed RNA polymerase, alpha subunit/40 kD subunit
Cluster125970	5.2	BDI3681 PRABACTJOH N3659 Pmer1199	COG0543 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases
Cluster86004	5.1	BDI0968	COG0141 Histidinol dehydrogenase COG0079 Histidinol-phosphate/aromatic aminotransferase and cobyrinic acid decarboxylase
Cluster19261	5.1	Csci0044	
Cluster146771	5.1	Bcap1947	COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Cluster74082	5.1	Aput2342	COG1060 Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes COG1427 Predicted periplasmic solute-binding protein
Cluster8146	5.1	BFych460987 BFnctc0908 Bfra31122704	COG2982 Uncharacterized protein involved in outer membrane biogenesis
Cluster12333	5.1	Acol1170	COG1372 Intein/homing endonuclease COG0209 Ribonucleotide reductase, alpha subunit
Cluster154885	5.1	Bhan2707	
Cluster173455	5.1	Csci3629	
Cluster183297	5.1	SB23peg3553	
Cluster195466	5.1	SB23peg1884	
Cluster21468	5.1	Csci3825	COG0514 Superfamily II DNA helicase
Cluster29826	5.1	SB23peg3675	COG0642 Signal transduction histidine kinase COG2202 FOG: PAS/PAC domain COG5002 Signal transduction histidine kinase COG2770 FOG: HAMP domain
Cluster814	5.1	Rtor0552	COG3669 Alpha-L-fucosidase
Cluster94474	5.1	SB23peg1355	COG1073 Hydrolases of the alpha/beta superfamily
Cluster19591	5.1	CspM6212903 Csym2680	COG0028 Thiamine pyrophosphate-requiring enzymes [acetolactate synthase, pyruvate dehydrogenase (cytochrome), glyoxylate carboligase, phosphonopyruvate decarboxylase]
Cluster133607	5.0	Rtor1105	COG0489 ATPases involved in chromosome partitioning COG3944 Capsular polysaccharide biosynthesis protein
Cluster156235	5.0	Svar1484	COG0087 Ribosomal protein L3
Cluster190016	5.0	Csci3345	
Cluster34847	5.0	Acol0356	COG1129 ABC-type sugar transport system, ATPase component COG3845 ABC-type uncharacterized transport systems, ATPase components
Cluster74775	5.0	Acol3131	COG0206 Cell division GTPase
Cluster1454	5.0	Aput1109	COG0086 DNA-directed RNA polymerase, beta' subunit/160 kD subunit
Cluster145931	5.0	Csci3339	
Cluster160242	5.0	SB23peg2307	COG2135 Uncharacterized conserved protein
Cluster197189	5.0	SB23peg2800	COG0346 Lactoylglutathione lyase and related lyases
Cluster23239	5.0	Aput1174	COG0517 FOG: CBS domain COG0589 Universal stress protein UspA and related nucleotide-binding proteins COG0038 Chloride channel protein ErC
Cluster32767	5.0	BDI1439	COG0737 5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases COG3103 SH3 domain protein COG4085 Predicted RNA-binding protein, contains TRAM domain COG1652 Uncharacterized protein containing LysM domain
Cluster112287	5.0	Rtor1199	COG3103 SH3 domain protein COG0860 N-acetylmuramoyl-L-alanine amidase COG2247 Putative cell wall-binding domain
Cluster72145	5.0	Chyl2278 Cspo2660 Dion1166	COG0006 Xaa-Pro aminopeptidase
Cluster3436	4.9	BVU4071 Bdor0680	COG0793 Periplasmic protease COG1506 Dipeptidyl aminopeptidases/acylaminoacyl-peptidases COG4946 Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system COG0823 Periplasmic component of the Tol biopolymer transport system COG1228 Imidazolonepropionase and related amidohydrolases COG3710 DNA-binding winged-HTH domains
Cluster132373	4.9	SB23peg3172	

Cluster85576	4.9	BVU1601 BFych463454 BFnctc3275 Bcoproc0260 Bcoprop1060 Bdor2167 Bfra31120281 Bple1348	COG0611 Thiamine monophosphate kinase COG0309 Hydrogenase maturation factor
Cluster11069	4.9	BDI1272	COG3525 N-acetyl-beta-hexosaminidase COG3537 Putative alpha-1,2-mannosidase
Cluster108523	4.8	BDI3299	COG5464 Uncharacterized conserved protein
Cluster12282	4.8	Rumhyd1340	COG1529 Aerobic-type carbon monoxide dehydrogenase, large subunit CoxL/CutL homologs COG2080 Aerobic-type carbon monoxide dehydrogenase, small subunit CoxS/CutS homologs COG4631 Xanthine dehydrogenase, molybdopterin-binding subunit B COG3427 Uncharacterized conserved protein
Cluster60444	4.8	Aput2062	COG1894 NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit COG4624 Iron only hydrogenase large subunit, C-terminal domain COG1034 NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G) COG0493 NADPH-dependent glutamate synthase beta chain and related oxidoreductases COG1142 Fe-S-cluster-containing hydrogenase components 2 COG0543 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases
Cluster63802	4.8	Bcac0449	
Cluster61662	4.7	BFych462718 BFnctc2733	
Cluster150874	4.7	Svar0857	COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain
Cluster201779	4.7	b3781 EFER3723 Csp3471 Ecan0963 Pret0257 Pstu3303	COG0526 Thiol-disulfide isomerase and thioredoxins COG3118 Thioredoxin domain-containing protein
Cluster150643	4.7	Csci0691	COG0274 Deoxyribose-phosphate aldolase
Cluster66811	4.6	Svar0380	COG0206 Cell division GTPase
Cluster125828	4.6	SB23peg246	COG0652 Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family COG0561 Predicted hydrolases of the HAD superfamily COG4696 Uncharacterized protein conserved in bacteria
Cluster14239	4.6	SB23peg2538	
Cluster10489	4.6	BFych463819 BFnctc3611 Bfra31121128	COG1409 Predicted phosphohydrolases COG1501 Alpha-glucosidases, family 31 of glycosyl hydrolases COG3525 N-acetyl-beta-hexosaminidase COG3537 Putative alpha-1,2-mannosidase
Cluster176249	4.6	SB23peg3171	COG2256 ATPase related to the helicase subunit of the Holliday junction resolvase COG2110 Predicted phosphatase homologous to the C-terminal domain of histone macroH2A1
Cluster22211	4.6	BactD21335	
Cluster25037	4.6	SB23peg3083	COG1410 Methionine synthase I, cobalamin-binding domain COG0646 Methionine synthase I (cobalamin-dependent), methyltransferase domain COG0685 5,10-methylenetetrahydrofolate reductase COG2040 Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)
Cluster34978	4.6	Rtor2559	
Cluster48693	4.6	SB23peg2293	COG4668 Mannitol/fructose-specific phosphotransferase system, IIA domain COG2213 Phosphotransferase system, mannitol-specific IIBC component
Cluster54993	4.6	SB23peg2954	COG0621 2-methylthioadenine synthetase
Cluster62782	4.6	Bhan1808	COG0446 Uncharacterized NAD(FAD)-dependent dehydrogenases COG1251 NAD(P)H-nitrite reductase COG2146 Ferredoxin subunits of nitrite reductase and ring-hydroxylating dioxygenases
Cluster99668	4.6	Rtor1700	COG0657 Esterase/lipase
Cluster135917	4.6	Acol3146	COG0217 Uncharacterized conserved protein
Cluster138426	4.6	SB23peg1357	COG0639 Diadenosine tetraphosphatase and related serine/threonine protein phosphatases
Cluster140057	4.6	SB23peg2666	COG0566 rRNA methylases
Cluster144984	4.6	SB23peg2067	
Cluster27900	4.6	Cbol4366 Chyl0566	COG2508 Regulator of polyketide synthase expression
Cluster34253	4.6	Rlac1669	COG0063 Predicted sugar kinase
Cluster56878	4.6	Csci0150	COG1316 Transcriptional regulator
Cluster62628	4.6	Rtor1198	COG0515 Serine/threonine protein kinase
Cluster118631	4.6	DpigATC0192 DpigGOR12386	COG0822 NifU homolog involved in Fe-S cluster formation
Cluster99569	4.6	FpraM2121060	
Cluster125520	4.5	Aput1523	COG0781 Transcription termination factor
Cluster52991	4.5	BDI3177	COG0739 Membrane proteins related to metalloendopeptidases COG4942 Membrane-bound metallopeptidase
Cluster7045	4.5	BDI3699 PRABACTJOHN3640 Pmer1183	COG4775 Outer membrane protein/protective antigen OMA87
Cluster155219	4.5	Rtor0865	COG0637 Predicted phosphatase/phosphohexomutase COG1554 Trehalose and maltose hydrolases (possible phosphorylases) COG1214 Inactive homolog of metal-dependent proteases, putative molecular chaperone COG0546 Predicted phosphatases
Cluster31413	4.5	Bhan1029 CspM6212964 Csym0986	COG2986 Histidine ammonia-lyase
Cluster9662	4.5	Acol0673	COG0466 ATP-dependent Lon protease, bacterial type
Cluster55437	4.5	Acol2330	COG0201 Preprotein translocase subunit SecY
Cluster178032	4.5	Csym2699 Csym2884	
Cluster62229	4.5	CspM6211953 Csym2932	COG1914 Mn2+ and Fe2+ transporters of the NRAMP family

Cluster4978	4.3	Casp3046 Cbol2801	COG1894 NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit COG4624 Iron only hydrogenase large subunit, C-terminal domain COG1034 NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G) COG1145 Ferredoxin COG0493 NADPH-dependent glutamate synthase beta chain and related oxidoreductases COG1142 Fe-S-cluster-containing hydrogenase components 2 COG0543 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases COG1148 Heterodisulfide reductase, subunit A and related polyferredoxins COG1319 Aerobic-type carbon monoxide dehydrogenase, middle subunit CoxM/CutM homologs COG1144 Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, delta subunit
Cluster224870	4.3	SB23peg2981	
Cluster17707	4.3	BT2694 BVU0333 BFYch464148 BFNctc3970 BDI3644 BWH20043 Bcel2307 Bdor0098 Begg2601 Bfra31120796 Bint1710 Bova0736 BactD14479 Bthe3731263 Bthe7330401 Buni0597 Bxyl1654 PRABACTJOHN3708 Pmer1238	COG2987 Urocanate hydratase
Cluster29051	4.2	BVU3027 Bdor2642	COG0318 Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II COG1022 Long-chain acyl-CoA synthetases (AMP-forming)
Cluster159471	4.2	Aput0536	
Cluster174657	4.2	Aput1820	
Cluster33263	4.2	SB23peg4017	COG0517 FOG: CBS domain COG0589 Universal stress protein UspA and related nucleotide-binding proteins COG0038 Chloride channel protein ErIC
Cluster118815	4.2	BVU1641 Bdor0235	COG1408 Predicted phosphohydrolases COG3326 Predicted membrane protein
Cluster12267	4.1	DpigATC0187 DpigGOR12390	COG1372 Intein/homing endonuclease COG1328 Oxygen-sensitive ribonucleoside-triphosphate reductase
Cluster131273	4.1	SB23peg1629	COG0561 Predicted hydrolases of the HAD superfamily
Cluster103129	4.1	Casp2317 Csym0678	COG2207 AraC-type DNA-binding domain-containing proteins COG3449 DNA gyrase inhibitor COG3708 Uncharacterized protein conserved in bacteria
Cluster135821	4.1	Rtor1241	COG1132 ABC-type multidrug transport system, ATPase and permease components COG1136 ABC-type antimicrobial peptide transport system, ATPase component COG3842 ABC-type spermidine/putrescine transport systems, ATPase components COG3839 ABC-type sugar transport systems, ATPase components COG1126 ABC-type polar amino acid transport system, ATPase component COG1125 ABC-type proline/glycine betaine transport systems, ATPase components COG1122 ABC-type cobalt transport system, ATPase component COG1137 ABC-type (unclassified) transport system, ATPase component COG1118 ABC-type sulfate/molybdate transport systems, ATPase component COG0396 ABC-type transport system involved in Fe-S cluster assembly, ATPase component COG0411 ABC-type branched-chain amino acid transport systems, ATPase component
Cluster157167	4.1	Ecan2245	COG0583 Transcriptional regulator
Cluster171428	4.1	SB23peg722	
Cluster196272	4.1	DpigATC1798 DpigGOR11868	COG0048 Ribosomal protein S12
Cluster201627	4.1	DpigATC2191 DpigGOR11454	COG0198 Ribosomal protein L24
Cluster220435	4.1	Bhan0504	
Cluster28302	4.1	Cbol2364	COG3858 Predicted glycosyl hydrolase
Cluster33908	4.1	SB23peg3448	
Cluster3479	4.1	SB23peg2278	COG0553 Superfamily II DNA/RNA helicases, SNF2 family COG4279 Uncharacterized conserved protein
Cluster52844	4.1	Csym3203	
Cluster56280	4.1	SB23peg1544	COG0006 Xaa-Pro aminopeptidase
Cluster115221	4.1	Bryfor0312 Cnex0545	COG1131 ABC-type multidrug transport system, ATPase component COG4555 ABC-type Na ⁺ transport system, ATPase component COG4152 ABC-type uncharacterized transport system, ATPase component COG4586 ABC-type uncharacterized transport system, ATPase component
Cluster62574	4.1	SB23peg1041	COG0826 Collagenase and related proteases
Cluster65194	4.1	BFYch464489 BFNctc4284 Bfra31120547	
Cluster73386	4.1	Aput0444	COG0763 Lipid A disaccharide synthetase COG3952 Predicted membrane protein
Cluster92170	4.1	DpigATC2366 DpigGOR11120	COG1180 Pyruvate-formate lyase-activating enzyme
Cluster97102	4.1	Cste0415	
Cluster46264	4.1	Csci3121	COG3681 Uncharacterized conserved protein
Cluster99597	4.0	SB23peg2628	COG1493 Serine kinase of the HPr protein, regulates carbohydrate metabolism
Cluster116682	4.0	Aput1563	COG0052 Ribosomal protein S2
Cluster16519	4.0	BDI1854 PRABACTJOHN2472 Pmer3192	COG0465 ATP-dependent Zn proteases
Cluster8369	4.0	Edol1377 SB23peg2867	COG0542 ATPases with chaperone activity, ATP-binding subunit
Cluster167035	-4.1	Rbro0231	COG1309 Transcriptional regulator
Cluster22201	-4.5	Begg2361	

Cluster91423	-5.0	BT2510 BFych460541 BFnctc0489 Bcac2172 Bfin2282 Bfra31121966 Bova1155 Bsp1160514 BactD11151 BactD20321 Bthe3732525 Bthe7332673 Bxyl1549	COG0039 Malate/lactate dehydrogenases
Cluster180217	-5.2	BT4586 BVU3826 BWH22906 Bcac0064 Bcel3226 Bdor1189 Begg1336 Bfin3414 Bint3701 BactD10717 Bste0771 Bthe3735364 Bthe7334501 Bxyl3412 Pmer0365	COG0537 Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases
Cluster1412	-5.6	Bova2727 BactD12411 BactD21917 Bxyl4428	COG0642 Signal transduction histidine kinase COG2202 FOG: PAS/PAC domain COG0784 FOG: CheY-like receiver COG5002 Signal transduction histidine kinase COG3292 Predicted periplasmic ligand-binding sensor domain COG0834 ABC-type amino acid transport/signal transduction systems, periplasmic component/domain COG3322 Predicted periplasmic ligand-binding sensor domain COG4753 Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain COG2972 Predicted signal transduction protein with a C-terminal ATPase domain COG1879 ABC-type sugar transport system, periplasmic component COG2114 Adenylate cyclase, family 3 (some proteins contain HAMP domain) COG4251 Bacteriophytochrome (light-regulated signal transduction histidine kinase) COG2770 FOG: HAMP domain COG2172 Anti-sigma regulatory factor (Ser/Thr protein kinase)
Cluster51773	-5.6	BWH20596 Bcel1792 Bint0973	COG3507 Beta-xylosidase COG5498 Predicted glycosyl hydrolase COG3940 Predicted beta-xylosidase
Cluster57697	-7.0	BVU0182 BWH24340 Bcel2822 Bdor0327 Bint4068	COG2755 Lysophospholipase L1 and related esterases COG4677 Pectin methyltransferase COG3401 Fibronectin type 3 domain-containing protein
Cluster69747	-7.2	BT0556 Begg2561 Bfin1963 Bint1818 Bova2850 BactD10824 BactD20410 Bthe3734188 Bthe7335317 Bxyl0105	COG0505 Carbamoylphosphate synthase small subunit
Cluster114095	-7.8	BWH20411 Bcel1942 Begg2823 Bint1406 Bste1842 Buni3186	COG0545 FKBP-type peptidyl-prolyl cis-trans isomerases 1
Cluster32640	-7.9	BD11579	COG5360 Uncharacterized protein conserved in bacteria
Cluster67314	-8.5	Bova1548 BactD142871 BactD22945 Bxyl1818	COG4292 Predicted membrane protein
Cluster143617	-9.2	BT0157 Bcac0190 Bfin0743 Bova0923 Bsp116109 BactD13010 BactD23789 Bthe3733749 Bthe7334688 Bxyl3820	
Cluster1409	-10.1	BT3738 Bcac3036 Bdor4231 Begg1729 Bint3489 Bsp1161420 BactD11073 Bthe3732689 Bthe7332858 Bxyl1623	COG0642 Signal transduction histidine kinase COG2198 FOG: HPT domain COG2202 FOG: PAS/PAC domain COG0784 FOG: CheY-like receiver COG5002 Signal transduction histidine kinase COG3292 Predicted periplasmic ligand-binding sensor domain COG0834 ABC-type amino acid transport/signal transduction systems, periplasmic component/domain COG2203 FOG: GAF domain COG3437 Response regulator containing a CheY-like receiver domain and an HD-GYP domain COG5278 Predicted periplasmic ligand-binding sensor domain COG3322 Predicted periplasmic ligand-binding sensor domain COG4252 Predicted transmembrane sensor domain COG4753 Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain COG2197 Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain COG4977 Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain COG2972 Predicted signal transduction protein with a C-terminal ATPase domain COG1879 ABC-type sugar transport system, periplasmic component COG2114 Adenylate cyclase, family 3 (some proteins contain HAMP domain) COG4251 Bacteriophytochrome (light-regulated signal transduction histidine kinase) COG2770 FOG: HAMP domain COG2207 AraC-type DNA-binding domain-containing proteins COG3452 Predicted periplasmic ligand-binding sensor domain COG2201 Chemotaxis response regulator containing a CheY-like receiver domain and a methyltransferase domain COG2172 Anti-sigma regulatory factor (Ser/Thr protein kinase)
Cluster78565	-10.2	BWH20367 Bcel1979	

Cluster41689	-10.5	BT0825 BVU3075 BWH21280 Bcel4050 Bdor2584 Bova1917 Bple1462 BactD10540 BactD20772 Bthe3734668 Bthe7333994 Bxyl0493	COG1028 Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) COG1070 Sugar (pentulose and hexulose) kinases COG0246 Mannitol-1-phosphate/altronate dehydrogenases
Cluster10993	-10.6	Bova0633 BactD12240 BactD21690 Bxyl4083	COG0642 Signal transduction histidine kinase COG2198 FOG: HPT domain COG0834 ABC-type amino acid transport/signal transduction systems, periplasmic component/domain COG2203 FOG: GAF domain COG3300 MHYT domain (predicted integral membrane sensor domain) COG3452 Predicted periplasmic ligand-binding sensor domain COG3614 Predicted periplasmic ligand-binding sensor domain COG3447 Predicted integral membrane sensor domain COG4252 Predicted transmembrane sensor domain
Cluster1260	-10.7	BWH20597 Bcel1791 Bint0974	COG0642 Signal transduction histidine kinase COG2202 FOG: PAS/PAC domain COG0784 FOG: CheY-like receiver COG5002 Signal transduction histidine kinase COG3292 Predicted periplasmic ligand-binding sensor domain COG4252 Predicted transmembrane sensor domain COG4753 Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain COG3706 Response regulator containing a CheY-like receiver domain and a GGDEF domain COG5001 Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain COG0745 Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain COG1879 ABC-type sugar transport system, periplasmic component COG2114 Adenylate cyclase, family 3 (some proteins contain HAMP domain) COG4251 Bacteriophytochrome (light-regulated signal transduction histidine kinase)
Cluster16935	-11.3	BWH25316 Bcel1456 Bint0448	COG1752 Predicted esterase of the alpha-beta hydrolase superfamily COG4775 Outer membrane protein/protective antigen OMA87
Cluster47058	-13.5	Ccom0399	COG1653 ABC-type sugar transport system, periplasmic component
Cluster5283	-18.7	Bcoprop2883	
Cluster187979	-18.8	BFych462625 BFnctc2646 BWH21128 BactD10814	COG0071 Molecular chaperone (small heat shock protein)
Cluster10946	-23.8	Bcoproc0252 Bcoproc0670 Bcoprop0596 Bova1991 BactD22776	COG1472 Beta-glucosidase-related glycosidases
Cluster23352	-68.8	Bxyl0325	COG0793 Periplasmic protease

*Significant genes were identified using Cyber-T with the following criteria: p-value<0.001, PPDE(<p)>0.95, fold-change≥4, and ≥1 sequence observed in all samples from the up-regulated group.